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## REPLACEMENT SHEET

Fig. 1A

Restriction map of plasmid ms23

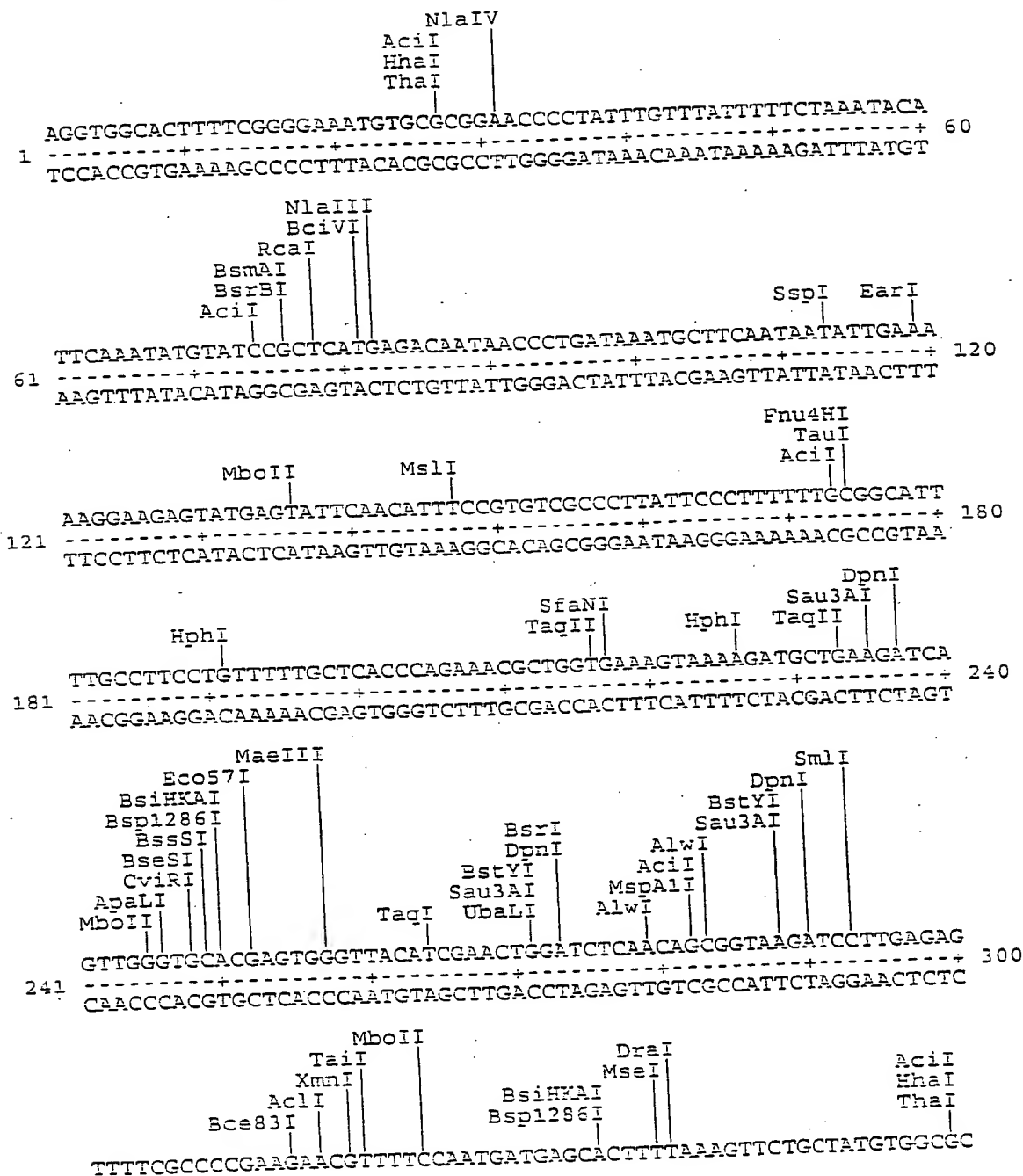


Fig. 1A (cont.)

## 2/21 REPLACEMENT SHEET

**A**

301 +-----+-----+-----+-----+-----+-----+-----+ 360  
AAAAGCGGGCTTCTTGCAAAAGGTTACTACTCGTGAAAATTTCAAGACGATA CACC GCG

HgaI  
TaqII  
NciI  
ScrFI  
MspI  
BcgI  
HpaI  
BsaHI  
BscGI  
Fnu4HI  
TauI  
Acil  
BseMIII  
DdeI  
Bgcl

361 GGTATTATCCCGTATTGACGCCGGGAAGAGCAACTCGGTTCGCCGCATACACTATTCTCA 420  
- - - - -  
CCATAATAGGGCATAA CTGCGGCCCC GTTCTCGTTGAGCCAG CGGCGT ATGTGATA AGAGT

Rsal  
ScaI  
MaeIII  
TatI  
HphI  
Tspl  
BsrI  
BccI  
SfaNI  
NlaIII  
FokI  
Bst4CI

421 GAATGACTTGGTTGAGTACTCACAGAAAAAGCATCTTACGGATGGCATGACAGT 480  
- - - - -  
CTTACTGAACCA ACTCATGAGTGGT CAGTGTCT TTTTCGTAGA ATGCCT ACCGTACTGT CA

CviJI  
HaeIII  
TspRI  
EaeI  
Fnu4HI  
GdiII  
TauI  
Acil  
BtsI  
CjePI  
Tsp509I  
BbvI  
CvirI  
BtsI  
TseI  
Fnu4HI  
TspRI  
Msll  
NlaIII

481 AAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAAACACTGCGGCCAACTTACTTCT 540  
- - - - -  
TTCTCTTAATACG TCACGACGGT ATTGGTACTCA CTATTGTG ACGCCGGT TGAATGAAGA

AvaII  
Sau96I  
CjePI  
BsiEI  
PvuI  
DpnI  
Sau3AI  
MnlI  
AluI  
QacII  
CviJI  
CviRl  
NlaIII  
Sau3AI  
DpnI  
NlaIII  
MaeIII  
AlwI

541 GACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGT 600  
- - - - -  
CTGTTGCTAGCCTCCTGGCTTCCTCGATTGGCGAAAAACGTGTTGTACCCCCTAGTACA

AceIII  
DpnI  
Sau3AI  
MspI  
BsawI  
NlaIV  
AluI  
CviJI  
CviJl  
Sfani  
MaeIII  
Tsp45I

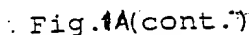
601 AA CTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGA 660  
- - - - -  
TTGAGCGGA ACTAGCAACCCT TGGCCTCGACTTACTTCGGTATGGTTTGCTGCTCGCACT

MslI  
SfcI  
BsrDI  
AclI  
Tail  
HhaI  
FspI  
MseI  
BsrI

661 CACCACGATGCCTGTAGCAATTGGCAACAACGTTGCGCAA ACTATTA ACTGGCGAACTACT 720  
- - - - -  
GTGGTGCTACCGACATCGTTACC GTTGT TGCAACGCGTTTGATAATTGACCGCTTGTATGA

MSEI





1081 TAATCTCATGACCAAAATCCCTTAAACGTGAGTTCGTTCCACTGAGCGTCAGACCCCGT 1140  
 ATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCA

DpnI  
 BstYI  
 Sau3AI  
 MboII  
 DpnI  
 Sau3AI  
 CjeI  
 CjePI  
 Bsp24I  
 DpnI  
 BstYI  
 Sau3AI  
 AlwI  
 SmlI  
 AlwI  
 DpnI  
 Tth111II  
 Sca83I  
 RhaI  
 ThaI  
 BbvI  
 CviRI  
 Cac8I  
 Fnu4HI  
 TseI  
 MwoI

AGAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGGTAATCTGCTGCTTGCA  
 TCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGT

1141 1200

HgiEII  
 AciII  
 MspAII  
 Tth111III  
 Tth111III  
 CjeI  
 CjeI  
 CjeI  
 CjeI  
 DpnI  
 Sau3AI  
 MspI  
 AluI  
 CviII  
 AlwI  
 CjePI

AACAAAAAACACCGCTACCAGCGGTGGTGGTTTGGCCGGATCAAGAGCTACCAACTCT  
 TTGTTTTTTTTTGGTGGCGATGGTCGCCACCAAAACAAACGGCCTAGTTCTCGATGGTTGAGA

1201 1260

Eco57I    MaeIII    BsrI    CviJI    CjePI    HhaI    Bsp24I    CjePI    CjeI    BceFI    Bst4CI    BfaI  
 TTTTCCGAAGGTTAACTGGCTTCAGCAGAGCGCAGATACCAATACTGTCTCTTAGTGTA  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 AAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACAT

1261 1320

CjaI CviJI  
 CjePI HaeI  
 Bsp24I HaeIII  
 CviJI BslI SfiI AclI MnlI  
 1321 GCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCT 1330  
 -----+-----+-----+-----+-----+  
 CGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGA

BbvI      MaeIII    BbvI    BsrI    Fnu4HI    TspRI    AlwNI    CviJI    TseI    BsrI  
              BbvI    BsrI    Fnu4HI    TspRI    MmeI    TspRI    Bce83I    PstI    NciI    ScrFI    MspI    HinfI    SmaI  
 AATCCTGTTACCAAGTGGCTGCTGCCAGTGCGATAAGTCGTGTCTTACCGGGTTGGACTC  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----  
 TTAGGACAATTGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCCAACCTGAG

1381

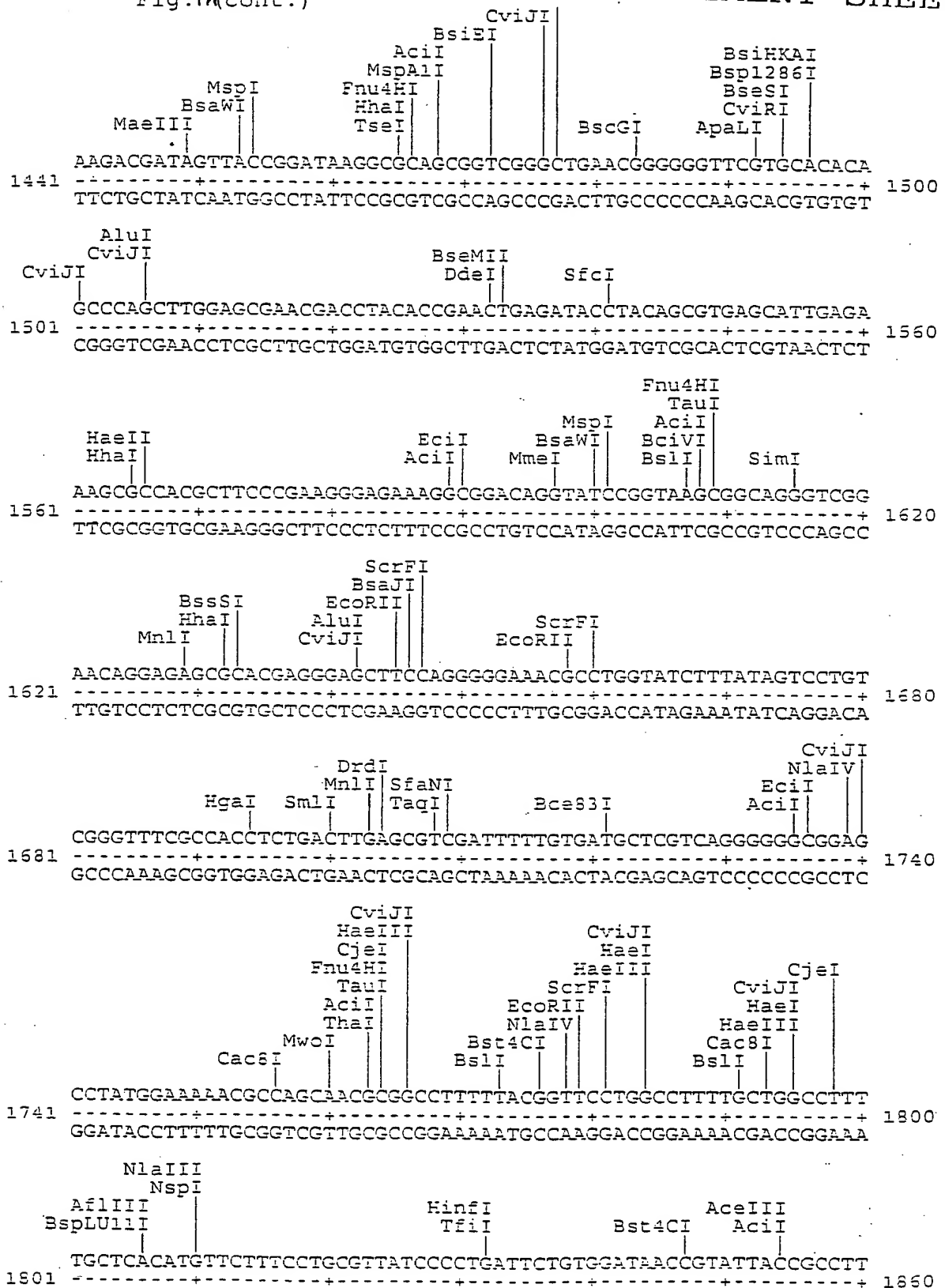
1440

END



Fig.1A(cont.)

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## 6/21 REPLACEMENT SHEET

Fig.1A(cont.)

ACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGAA

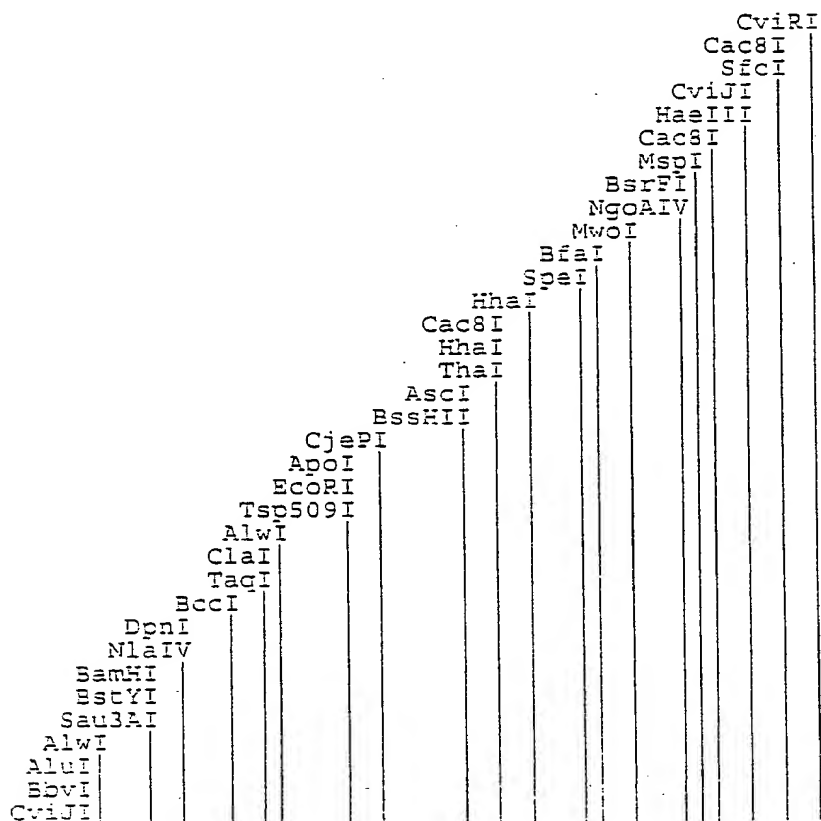
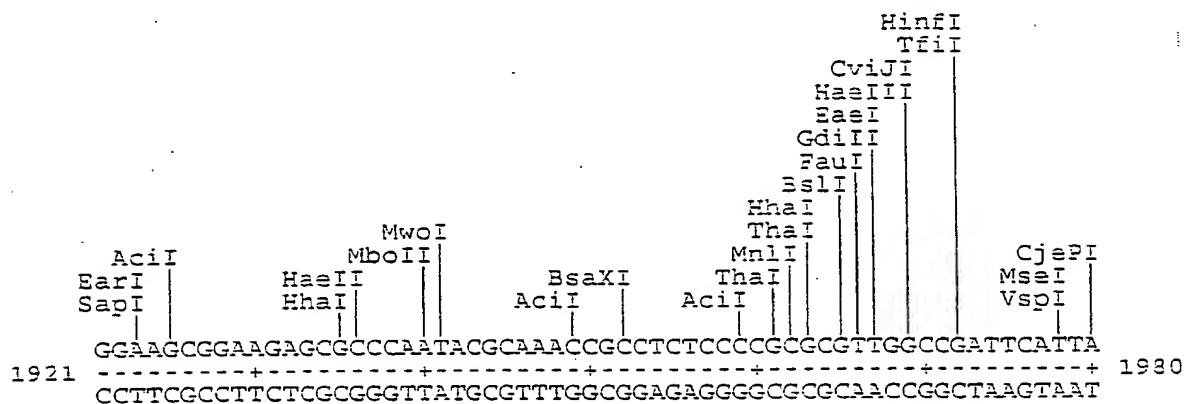
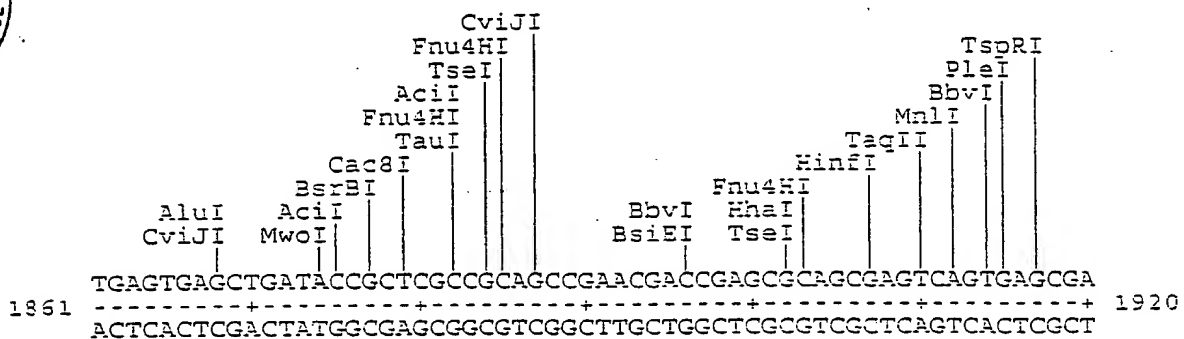
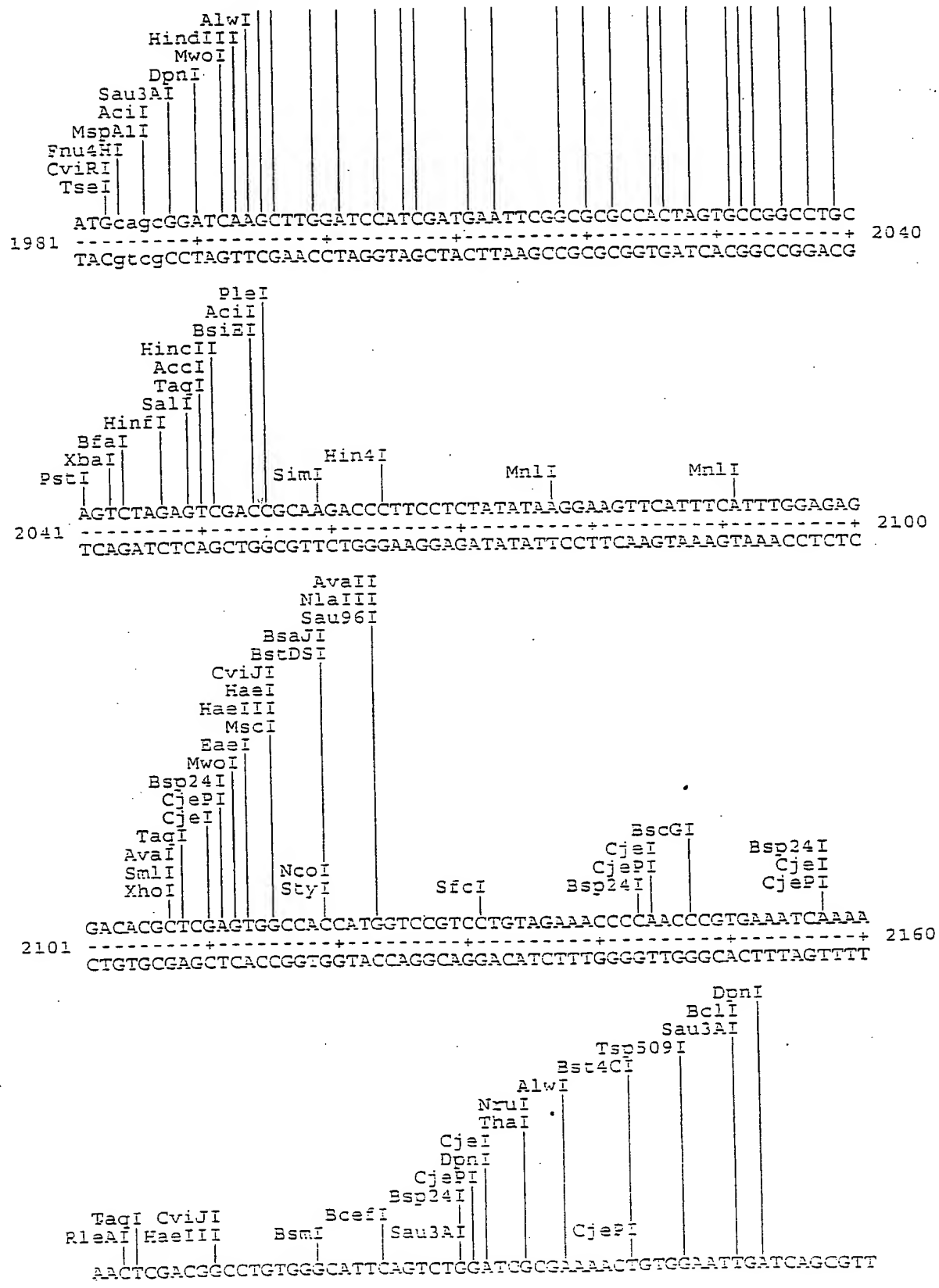




Fig.1A(cont.)









## 9/21 REPLACEMENT SHEET

Fig. 1A(cont.)

2641 TAATGCTCTACACCACGCCGAACACCTGGGTGGACGATATCACCGTGGTGACGCATGTGCG 2700  
ATTACGAGATGTGGTGGCGCTTGTGGACCCACCTGCTATAGTGGCACCCTGCGTACAGC

2701 CCAAGACTGTAACCACGCGTCTGTTGACTGGCAGGTGGTGGCCAATGGTGATGTCTAGCGG 2760  
GCGTTCTGACATTGGTGCGCAGACAACCTGACCGTCCACCACCGGTTACCACTACAGTCGC

2761 TTGAAGTGGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTAGCGGGACTT 2820  
AACTTGACGCACTACGCCTAGTTGTCCACCAACGTTGACCTGTTCCGTGATCGCCCTGAA

2821 TGCAAGTGGTGAATCCGCACCTCTGGCAACCGGGTGAAGGTTATCTCTATGAAGTGTGCG 2880  
ACGTTCAACCACTTAGGCGTGGAGACCGTTGGCCCACTTCCAATAGAGATACTTGACACGC

2891 TCACAGCCAAAAGCCAGACAGAGTGTGATATCTACCCGCTTCGCGTCGGCATCCGGTTCAG 2940  
AGTGTGCGGTTTTTCGGTCTGTCTCACACTATAGATGGGCGAAGCGCAGCCGTAGGCCAGTC

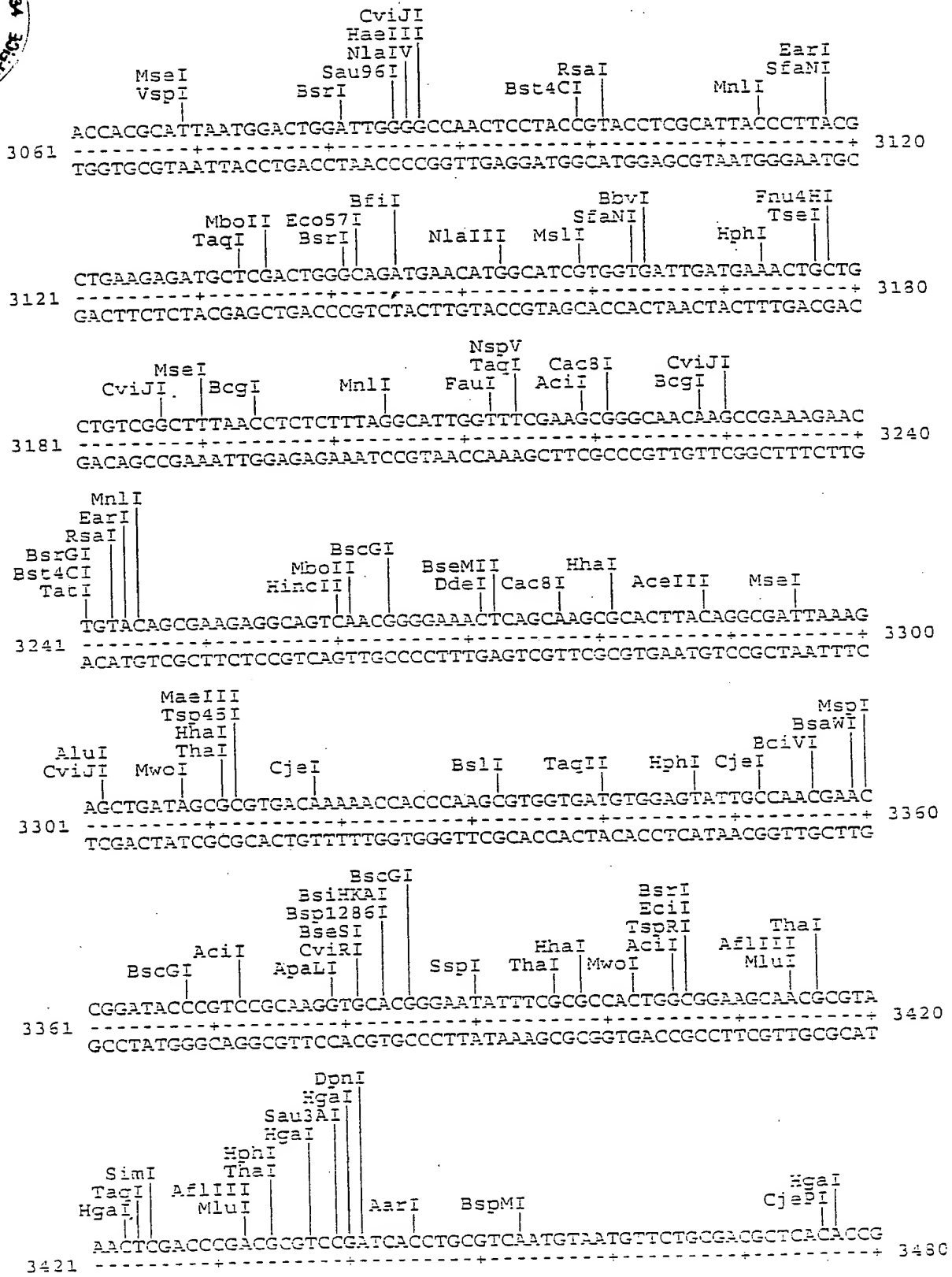
2941 TGGCAGTGAAGGGCGAACAGTTCCTGATTAACCACAAACCGTTCTACTTTACTGGCTTTG 3000  
ACCGTCACTTCCCGCTTGTCAAGGACTAATTGGTGTGTTGGCAAGATGAAATGACCGAAAC

3001 GTCGTCATGAAGATGCGGACTTGGCGTGGCAAGGATTGCGATAACGTGCTGATGGTGCACG 3060  
CAGCAGTACTTCTACGCCTGAACGCACCGTTTCTTAAGCTATTGCACGACTACCACGTGC



Fig.1A(cont.)

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# REPLACEMENT SHEET

Fig. 1A(cont.)

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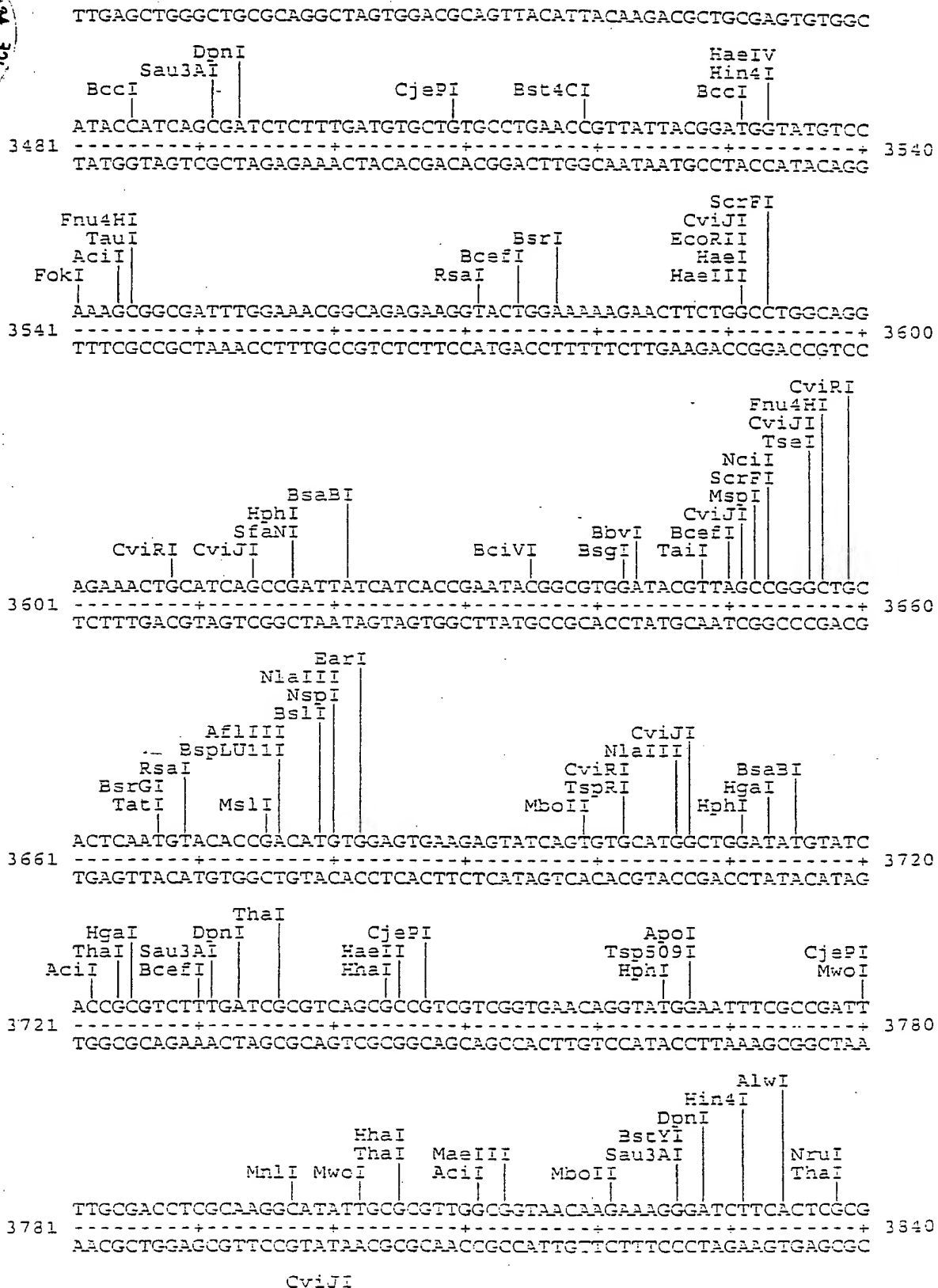
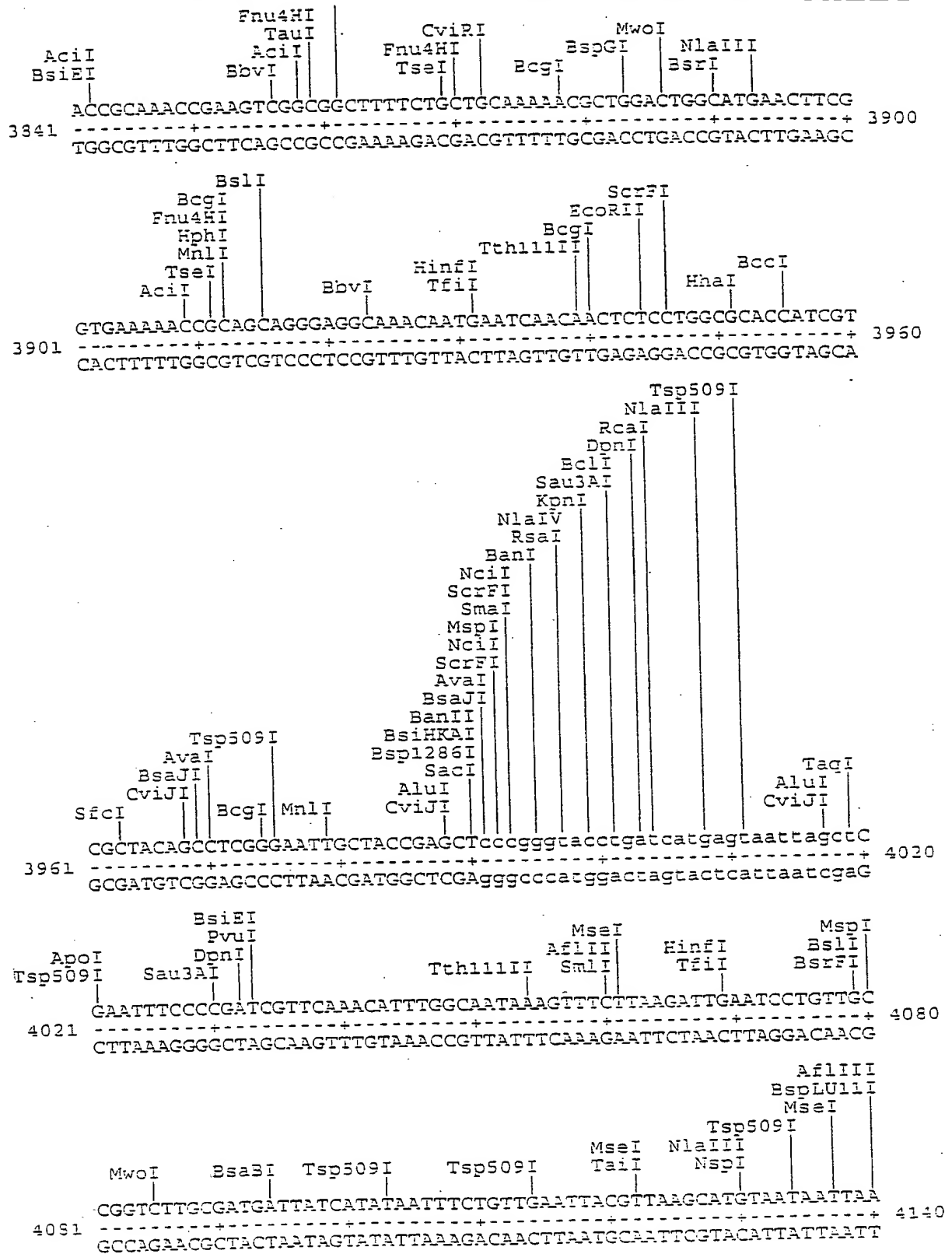




Fig.1A(cont.)

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## REPLACEMENT SHEET







# REPLACEMENT SHEET

pGPTV-GUS-kan

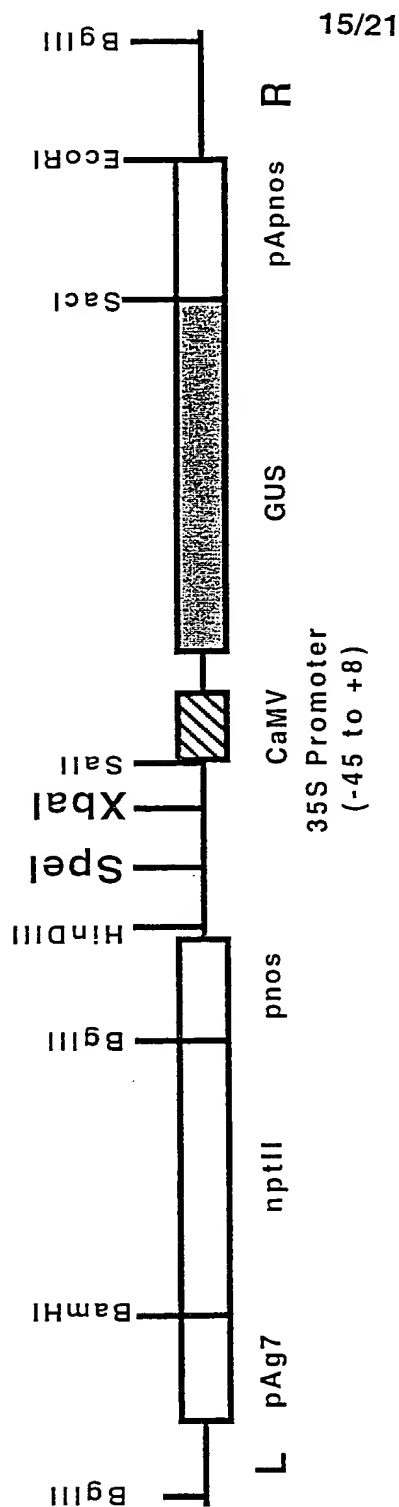


Fig. 3

# REPLACEMENT SHEET

Fig. 4

